

RECEIVED

JUL 20 2001

TECH CENTER 1600/2900

SEQUENCE LISTING

<110> Otsuka Pharmaceutical Co., Ltd.

<120> HUMAN P51 GENES AND GENE PRODUCTS THEREOF

<130> Q61014

<140> 09/670,568

<141> 2000-09-27

<150> JP 10-100467

<151> 1998-03-27

<160> 23

<170> PatentIn version 3.1

<210> 1

<211> 448

<212> PRT

<213> Homo sapiens

<220>

<221> DOMAIN

<222> (1)..(59)

<223> transactivation domain

<220>

<221> DNA_BIND

<222> (142)..(321)

<223> DNA binding domain

<220>

<221> DOMAIN

<222> (353)..(397)

<223> oligomerization domain

<400> 1

Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
1 5 10 15

Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
20 25 30

Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
35 40 45

Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
 50 55 60

Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
 65 70 75 80

Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
 85 90 95

Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
 100 105 110

Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
 115 120 125

Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
 130 135 140

Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
 145 150 155 160

Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
 165 170 175

Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
 180 185 190

Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
 195 200 205

Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
 210 215 220

Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
 225 230 235 240

Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
 245 250 255

Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
 260 265 270

Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
275 280 285

Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
290 295 300

Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
305 310 315 320

Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
325 330 335

Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
340 345 350

Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
355 360 365

Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
370 375 380

Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
385 390 395 400

Gln Gln Gln His Gln His Leu Leu Gln Lys His Leu Leu Ser Ala Cys
405 410 415

Phe Arg Asn Glu Leu Val Glu Pro Arg Arg Glu Thr Pro Lys Gln Ser
420 425 430

Asp Val Phe Phe Arg His Ser Lys Pro Pro Asn Arg Ser Val Tyr Pro
435 440 445

<210> 2
<211> 2816
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (145) .. (1488)
<223>

<220>

<221> polyA_signal

<222> (2786)..(2791)

<223>

<400> 2

tcgttgatat caaagacagt tgaaggaaat gaattttgaa acttcacggt gtgccaccct 60

acagtactgc cctgaccctt acatccagcg tttcgtagaa acccagctca tttctcttgg 120

aaagaaagtt attaccgatc cacc atg tcc cag agc aca cag aca aat gaa 171

Met Ser Gln Ser Thr Gln Thr Asn Glu
1 5

ttc ctc agt cca gag gtt ttc cag cat atc tgg gat ttt ctg gaa cag 219

Phe Leu Ser Pro Glu Val Phe Gln His Ile Trp Asp Phe Leu Glu Gln
10 15 20 25

cct ata tgt tca gtt cag ccc att gac ttg aac ttt gtg gat gaa cca 267

Pro Ile Cys Ser Val Gln Pro Ile Asp Leu Asn Phe Val Asp Glu Pro
30 35 40

tca gaa gat ggt gcg aca aac aag att gag att agc atg gac tgt atc 315

Ser Glu Asp Gly Ala Thr Asn Lys Ile Glu Ile Ser Met Asp Cys Ile
45 50 55

cgc atg cag gac tcg gac ctg agt gac ccc atg tgg cca cag tac acg 363

Arg Met Gln Asp Ser Asp Leu Ser Asp Pro Met Trp Pro Gln Tyr Thr
60 65 70

aac ctg ggg ctc ctg aac agc atg gac cag cag att cag aac ggc tcc 411

Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn Gly Ser
75 80 85

tcg tcc acc agt ccc tat aac aca gac cac gcg cag aac agc gtc acg 459

Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser Val Thr
90 95 100 105

gcg ccc tcg ccc tac gca cag ccc agc tcc acc ttc gat gct ctc tct 507

Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala Leu Ser
110 115 120

cca tca ccc gcc atc ccc tcc aac acc gac tac cca ggc ccg cac agt 555

Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His Ser
125 130 135

ttc gac gtg tcc ttc cag cag tcg agc acc gcc aag tcg gcc acc tgg 603

Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp
140 145 150

acg tat tcc act gaa ctg aag aaa ctc tac tgc caa att gca aag aca 651

Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr
155 160 165

tgc ccc atc cag atc aag gtg atg acc cca cct cct cag gga gct gtt Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly Ala Val 170 175 180 185	699
atc cgc gcc atg cct gtc tac aaa aaa gct gag cac gtc acg gag gtg Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Glu Val 190 195 200	747
gtg aag cgg tgc ccc aac cat gag ctg agc cgt gaa ttc aac gag gga Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn Glu Gly 205 210 215	795
cag att gcc cct cct agt cat ttg att cga gta gag ggg aac agc cat Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn Ser His 220 225 230	843
gcc cag tat gta gaa gat ccc atc aca gga aga cag agt gtg ctg gta Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val Leu Val 235 240 245	891
cct tat gag cca ccc cag gtt ggc act gaa ttc acg aca gtc ttg tac Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val Leu Tyr 250 255 260 265	939
aat ttc atg tgt aac agc agt tgt gtt gga ggg atg aac cgc cgt cca Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro 270 275 280	987
att tta atc att gtt act ctg gaa acc aga gat ggg caa gtc ctg ggc Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly 285 290 295	1035
cga cgc tgc ttt gag gcc cgg atc tgt gct tgc cca gga aga gac agg Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg 300 305 310	1083
aag gcg gat gaa gat agc atc aga aag cag caa gtt tcg gac agt aca Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp Ser Thr 315 320 325	1131
aag aac ggt gat ggt acg aag cgc ccg ttt cgt cag aac aca cat ggt Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr His Gly 330 335 340 345	1179
atc cag atg aca tcc atc aag aaa cga aga tcc cca gat gat gaa ctg Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp Glu Leu 350 355 360	1227
tta tac tta cca gtg agg ggc cgt gag act tat gaa atg ctg ttg aag Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu Leu Lys 365 370 375	1275
atc aaa gag tcc ctg gaa ctc atg cag tac ctt cct cag cac aca att Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His Thr Ile	1323

380	385	390	
gaa acg tac agg caa cag caa cag cag cag cac cag cac tta ctt cag			1371
Glu Thr Tyr Arg Gln Gln Gln Gln Gln Gln His Gln His Leu Leu Gln			
395	400	405	
aaa cat ctc ctt tca gcc tgc ttc agg aat gag ctt gtg gag ccc cgg			1419
Lys His Leu Leu Ser Ala Cys Phe Arg Asn Glu Leu Val Glu Pro Arg			
410	415	420	425
aga gaa act cca aaa caa tct gac gtc ttc ttt aga cat tcc aag ccc			1467
Arg Glu Thr Pro Lys Gln Ser Asp Val Phe Phe Arg His Ser Lys Pro			
	430	435	440
cca aac cga tca gtg tac cca tagagcccta tctctatatt ttaagtgtgt			1518
Pro Asn Arg Ser Val Tyr Pro			
445			
gtgttggtatt tccatgtgta tatgtgagtg tgtgtgtgtg tatgtgtgtg cgtgtgtatc			1578
tagccctcat aaacaggact tgaagacact ttggctcaga gacccaactg ctcaaaggca			1638
caaagccact agtgagagaa tcttttgaag ggactcaaac ctttacaaga aaggatgttt			1698
tctgcagatt ttgtatcctt agaccggcca ttgggtgggtg aggaaccact gtgtttgtct			1758
gtgagctttc tgttgtttcc tgggagggag gggtcaggtg gggaaagggg cattaagatg			1818
tttattggaa cctttttctg tcttcttctg ttgtttttct aaaattcaca gggaagcttt			1878
tgagcaggtc tcaaacttaa gatgtctttt taagaaaagg agaaaaaagt tgttattgtc			1938
tgtgcataag taagtgttag gtgactgaga gactcagtca gaccctttta atgctgggtca			1998
tgtaataata ttgcaagtag taagaaacga aggtgtcaag tgtactgctg ggcagcgagg			2058
tgatcattac caaaagtaat caactttgtg ggtggagagt tctttgtgag aacttgcatt			2118
atgtgtgtcc tccctcatg tgtaggtaga acatttctta atgctgtgta cctgcctctg			2178
ccactgtatg ttggcatctg ttatgctaaa gtttttcttg tacatgaaac cctggaagac			2238
ctactacaaa aaaactgttg tttggccccc atagcaggtg aactcatttt gtgcttttaa			2298
tagaaagaca aatccacccc agtaatattg cccttacgta gttgtttacc attattcaaa			2358
gctcaaaata gaatttgaag ccctctcaca aaatctgtga ttaatttgct taattagagc			2418
ttctatccct caagcctacc taccataaaa ccagccatat tactgatact gttcagtgca			2478
tttagccagg agacttacgt tttgagtaag tgagatccaa gcagacgtgt taaaatcagc			2538
actcctggac tggaaattaa agattgaaag ggtagactac ttttcttttt tttactcaaa			2598
agtttagaga atctctgttt ctttccattt taaaaacata ttttaagata atagcataaa			2658

gacttttaaaa atgttcctcc cctccatctt cccacacca gtcaccagca ctgtattttc 2718
 tgtcaccaag acaatgattt cttgttattg aggctgttgc ttttgtggat gtgtgatttt 2778
 aattttcaat aaacttttgc atcttggttt aaaagaaa 2816

<210> 3
 <211> 448
 <212> PRT
 <213> Homo sapiens

<400> 3

Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
 1 5 10 15

Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
 20 25 30

Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
 35 40 45

Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
 50 55 60

Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
 65 70 75 80

Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
 85 90 95

Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
 100 105 110

Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
 115 120 125

Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
 130 135 140

Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
 145 150 155 160

Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
165 170 175

Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
180 185 190

Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
195 200 205

Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
210 215 220

Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
225 230 235 240

Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
245 250 255

Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
260 265 270

Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
275 280 285

Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
290 295 300

Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
305 310 315 320

Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
325 330 335

Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
340 345 350

Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
355 360 365

Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
370 375 380

Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
 385 390 395 400

Gln Gln Gln His Gln His Leu Leu Gln Lys His Leu Leu Ser Ala Cys
 405 410 415

Phe Arg Asn Glu Leu Val Glu Pro Arg Arg Glu Thr Pro Lys Gln Ser
 420 425 430

Asp Val Phe Phe Arg His Ser Lys Pro Pro Asn Arg Ser Val Tyr Pro
 435 440 445

<210> 4
 <211> 641
 <212> PRT
 <213> Homo sapiens

<220>
 <221> DOMAIN
 <222> (1)..(59)
 <223> transactivation domain

<220>
 <221> DNA_BIND
 <222> (142)..(321)
 <223> DNA binding domain

<220>
 <221> DOMAIN
 <222> (353)..(397)
 <223> oligomerization domain

<400> 4

Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
 1 5 10 15

Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
 20 25 30

Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
 35 40 45

Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu

50

55

60

Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
65 70 75 80

Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
85 90 95

Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
100 105 110

Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
115 120 125

Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
130 135 140

Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
145 150 155 160

Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
165 170 175

Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
180 185 190

Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
195 200 205

Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
210 215 220

Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
225 230 235 240

Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
245 250 255

Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
260 265 270

Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
275 280 285

Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
290 295 300

Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
305 310 315 320

Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
325 330 335

Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
340 345 350

Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
355 360 365

Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
370 375 380

Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
385 390 395 400

Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr Ser Ile Gln Ser
405 410 415

Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn Lys Met Asn Ser
420 425 430

Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg
435 440 445

Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met Gly Ala Asn Ile
450 455 460

Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp Met Asn Gly Leu
465 470 475 480

Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met Pro Ser Thr Ser
485 490 495

His Cys Thr Pro Pro Pro Pro Tyr Pro Thr Asp Cys Ser Ile Val Ser
 500 505 510

Phe Leu Ala Arg Leu Gly Cys Ser Ser Cys Leu Asp Tyr Phe Thr Thr
 515 520 525

Gln Gly Leu Thr Thr Ile Tyr Gln Ile Glu His Tyr Ser Met Asp Asp
 530 535 540

Leu Ala Ser Leu Lys Ile Pro Glu Gln Phe Arg His Ala Ile Trp Lys
 545 550 555 560

Gly Ile Leu Asp His Arg Gln Leu His Glu Phe Ser Ser Pro Ser His
 565 570 575

Leu Leu Arg Thr Pro Ser Ser Ala Ser Thr Val Ser Val Gly Ser Ser
 580 585 590

Glu Thr Arg Gly Glu Arg Val Ile Asp Ala Val Arg Phe Thr Leu Arg
 595 600 605

Gln Thr Ile Ser Phe Pro Pro Arg Asp Glu Trp Asn Asp Phe Asn Phe
 610 615 620

Asp Met Asp Ala Arg Arg Asn Lys Gln Gln Arg Ile Lys Glu Glu Gly
 625 630 635 640

Glu

<210> 5
 <211> 2270
 <212> DNA
 <213> Homo sapiens

<220>
 <221> exon
 <222> (145) .. (2067)
 <223>

<400> 5
 tcgttgatat caaagacagt tgaaggaaat gaattttgaa acttcacggt gtgccaccct

60

acagtactgc cctgaccctt acatccagcg tttcgtagaa acccagctca tttctcttgg	120
aaagaaagtt attaccgatc cacc atg tcc cag agc aca cag aca aat gaa	171
Met Ser Gln Ser Thr Gln Thr Asn Glu	
1 5	
ttc ctc agt cca gag gtt ttc cag cat atc tgg gat ttt ctg gaa cag	219
Phe Leu Ser Pro Glu Val Phe Gln His Ile Trp Asp Phe Leu Glu Gln	
10 15 20 25	
cct ata tgt tca gtt cag ccc att gac ttg aac ttt gtg gat gaa cca	267
Pro Ile Cys Ser Val Gln Pro Ile Asp Leu Asn Phe Val Asp Glu Pro	
30 35 40	
tca gaa gat ggt gcg aca aac aag att gag att agc atg gac tgt atc	315
Ser Glu Asp Gly Ala Thr Asn Lys Ile Glu Ile Ser Met Asp Cys Ile	
45 50 55	
cgc atg cag gac tcg gac ctg agt gac ccc atg tgg cca cag tac acg	363
Arg Met Gln Asp Ser Asp Leu Ser Asp Pro Met Trp Pro Gln Tyr Thr	
60 65 70	
aac ctg ggg ctc ctg aac agc atg gac cag cag att cag aac ggc tcc	411
Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn Gly Ser	
75 80 85	
tcg tcc acc agt ccc tat aac aca gac cac gcg cag aac agc gtc acg	459
Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser Val Thr	
90 95 100 105	
gcg ccc tcg ccc tac gca cag ccc agc tcc acc ttc gat gct ctc tct	507
Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala Leu Ser	
110 115 120	
cca tca ccc gcc atc ccc tcc aac acc gac tac cca ggc ccg cac agt	555
Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His Ser	
125 130 135	
ttc gac gtg tcc ttc cag cag tcg agc acc gcc aag tcg gcc acc tgg	603
Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp	
140 145 150	
acg tat tcc act gaa ctg aag aaa ctc tac tgc caa att gca aag aca	651
Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr	
155 160 165	
tgc ccc atc cag atc aag gtg atg acc cca cct cct cag gga gct gtt	699
Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly Ala Val	
170 175 180 185	
atc cgc gcc atg cct gtc tac aaa aaa gct gag cac gtc acg gag gtg	747
Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Glu Val	
190 195 200	
gtg aag cgg tgc ccc aac cat gag ctg agc cgt gaa ttc aac gag gga	795

Val	Lys	Arg	Cys	Pro	Asn	His	Glu	Leu	Ser	Arg	Glu	Phe	Asn	Glu	Gly		
			205					210					215				
cag	att	gcc	cct	cct	agt	cat	ttg	att	cga	gta	gag	ggg	aac	agc	cat	843	
Gln	Ile	Ala	Pro	Pro	Ser	His	Leu	Ile	Arg	Val	Glu	Gly	Asn	Ser	His		
		220					225					230					
gcc	cag	tat	gta	gaa	gat	ccc	atc	aca	gga	aga	cag	agt	gtg	ctg	gta	891	
Ala	Gln	Tyr	Val	Glu	Asp	Pro	Ile	Thr	Gly	Arg	Gln	Ser	Val	Leu	Val		
		235				240					245						
cct	tat	gag	cca	ccc	cag	gtt	ggc	act	gaa	ttc	acg	aca	gtc	ttg	tac	939	
Pro	Tyr	Glu	Pro	Pro	Gln	Val	Gly	Thr	Glu	Phe	Thr	Thr	Val	Leu	Tyr		
250					255					260					265		
aat	ttc	atg	tgt	aac	agc	agt	tgt	gtt	gga	ggg	atg	aac	cgc	cgt	cca	987	
Asn	Phe	Met	Cys	Asn	Ser	Ser	Cys	Val	Gly	Gly	Met	Asn	Arg	Arg	Pro		
				270					275					280			
att	tta	atc	att	gtt	act	ctg	gaa	acc	aga	gat	ggg	caa	gtc	ctg	ggc	1035	
Ile	Leu	Ile	Ile	Val	Thr	Leu	Glu	Thr	Arg	Asp	Gly	Gln	Val	Leu	Gly		
			285				290						295				
cga	cgc	tgc	ttt	gag	gcc	cgg	atc	tgt	gct	tgc	cca	gga	aga	gac	agg	1083	
Arg	Arg	Cys	Phe	Glu	Ala	Arg	Ile	Cys	Ala	Cys	Pro	Gly	Arg	Asp	Arg		
		300					305					310					
aag	gcg	gat	gaa	gat	agc	atc	aga	aag	cag	caa	gtt	tcg	gac	agt	aca	1131	
Lys	Ala	Asp	Glu	Asp	Ser	Ile	Arg	Lys	Gln	Gln	Val	Ser	Asp	Ser	Thr		
		315				320					325						
aag	aac	ggt	gat	ggt	acg	aag	cgc	ccg	ttt	cgt	cag	aac	aca	cat	ggt	1179	
Lys	Asn	Gly	Asp	Gly	Thr	Lys	Arg	Pro	Phe	Arg	Gln	Asn	Thr	His	Gly		
330					335					340					345		
atc	cag	atg	aca	tcc	atc	aag	aaa	cga	aga	tcc	cca	gat	gat	gaa	ctg	1227	
Ile	Gln	Met	Thr	Ser	Ile	Lys	Lys	Arg	Arg	Ser	Pro	Asp	Asp	Glu	Leu		
				350					355					360			
tta	tac	tta	cca	gtg	agg	ggc	cgt	gag	act	tat	gaa	atg	ctg	ttg	aag	1275	
Leu	Tyr	Leu	Pro	Val	Arg	Gly	Arg	Glu	Thr	Tyr	Glu	Met	Leu	Leu	Lys		
			365				370						375				
atc	aaa	gag	tcc	ctg	gaa	ctc	atg	cag	tac	ctt	cct	cag	cac	aca	att	1323	
Ile	Lys	Glu	Ser	Leu	Glu	Leu	Met	Gln	Tyr	Leu	Pro	Gln	His	Thr	Ile		
		380					385					390					
gaa	acg	tac	agg	caa	cag	caa	cag	cag	cag	cac	cag	cac	tta	ctt	cag	1371	
Glu	Thr	Tyr	Arg	Gln	Gln	Gln	Gln	Gln	Gln	His	Gln	His	Leu	Leu	Gln		
		395				400					405						
aaa	cag	acc	tca	ata	cag	tct	cca	tct	tca	tat	ggt	aac	agc	tcc	cca	1419	
Lys	Gln	Thr	Ser	Ile	Gln	Ser	Pro	Ser	Ser	Tyr	Gly	Asn	Ser	Ser	Pro		
410					415					420					425		

cct ctg aac aaa atg aac agc atg aac aag ctg cct tct gtg agc cag	1467
Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val Ser Gln	
430 435 440	
ctt atc aac cct cag cag cgc aac gcc ctc act cct aca acc att cct	1515
Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr Ile Pro	
445 450 455	
gat ggc atg gga gcc aac att ccc atg atg ggc acc cac atg cca atg	1563
Asp Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met Pro Met	
460 465 470	
gct gga gac atg aat gga ctc agc ccc acc cag gca ctc cct ccc cca	1611
Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro Pro Pro	
475 480 485	
ctc tcc atg cca tcc acc tcc cac tgc aca ccc cca cct ccg tat ccc	1659
Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro Tyr Pro	
490 495 500 505	
aca gat tgc agc att gtc agt ttc tta gcg agg ttg ggc tgt tca tca	1707
Thr Asp Cys Ser Ile Val Ser Phe Leu Ala Arg Leu Gly Cys Ser Ser	
510 515 520	
tgt ctg gac tat ttc acg acc cag ggg ctg acc acc atc tat cag att	1755
Cys Leu Asp Tyr Phe Thr Thr Gln Gly Leu Thr Thr Ile Tyr Gln Ile	
525 530 535	
gag cat tac tcc atg gat gat ctg gca agt ctg aaa atc cct gag caa	1803
Glu His Tyr Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro Glu Gln	
540 545 550	
ttt cga cat gcg atc tgg aag ggc atc ctg gac cac cgg cag ctc cac	1851
Phe Arg His Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln Leu His	
555 560 565	
gaa ttc tcc tcc cct tct cat ctc ctg cgg acc cca agc agt gcc tct	1899
Glu Phe Ser Ser Pro Ser His Leu Leu Arg Thr Pro Ser Ser Ala Ser	
570 575 580 585	
aca gtc agt gtg ggc tcc agt gag acc cgg ggt gag cgt gtt att gat	1947
Thr Val Ser Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val Ile Asp	
590 595 600	
gct gtg cga ttc acc ctc cgc cag acc atc tct ttc cca ccc cga gat	1995
Ala Val Arg Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro Arg Asp	
605 610 615	
gag tgg aat gac ttc aac ttt gac atg gat gct cgc cgc aat aag caa	2043
Glu Trp Asn Asp Phe Asn Phe Asp Met Asp Ala Arg Arg Asn Lys Gln	
620 625 630	
cag cgc atc aaa gag gag ggg gag tgagcctcac catgtgagct cttcctatcc	2097
Gln Arg Ile Lys Glu Glu Gly Glu	
635 640	

ctctcctaac tgccagcccc ctaaaagcac tcctgcttaa tcttcaaagc cttctcccta 2157
gctcctcccc ttcctcttgt ctgatttctt aggggaagga gaagtaagag gctacctctt 2217
acctaacatc tgacctggca tctaattctg attctggctt taagccttca aaa 2270

<210> 6
<211> 641
<212> PRT
<213> Homo sapiens

<400> 6

Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
1 5 10 15

Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
20 25 30

Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
35 40 45

Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
50 55 60

Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
65 70 75 80

Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
85 90 95

Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
100 105 110

Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
115 120 125

Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
130 135 140

Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
145 150 155 160

Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
 165 170 175

Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
 180 185 190

Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
 195 200 205

Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
 210 215 220

Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
 225 230 235 240

Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
 245 250 255

Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
 260 265 270

Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
 275 280 285

Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
 290 295 300

Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
 305 310 315 320

Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
 325 330 335

Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
 340 345 350

Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
 355 360 365

Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
 370 375 380

Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
 385 390 395 400

Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr Ser Ile Gln Ser
 405 410 415

Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn Lys Met Asn Ser
 420 425 430

Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg
 435 440 445

Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met Gly Ala Asn Ile
 450 455 460

Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp Met Asn Gly Leu
 465 470 475 480

Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met Pro Ser Thr Ser
 485 490 495

His Cys Thr Pro Pro Pro Pro Tyr Pro Thr Asp Cys Ser Ile Val Ser
 500 505 510

Phe Leu Ala Arg Leu Gly Cys Ser Ser Cys Leu Asp Tyr Phe Thr Thr
 515 520 525

Gln Gly Leu Thr Thr Ile Tyr Gln Ile Glu His Tyr Ser Met Asp Asp
 530 535 540

Leu Ala Ser Leu Lys Ile Pro Glu Gln Phe Arg His Ala Ile Trp Lys
 545 550 555 560

Gly Ile Leu Asp His Arg Gln Leu His Glu Phe Ser Ser Pro Ser His
 565 570 575

Leu Leu Arg Thr Pro Ser Ser Ala Ser Thr Val Ser Val Gly Ser Ser
 580 585 590

Glu Thr Arg Gly Glu Arg Val Ile Asp Ala Val Arg Phe Thr Leu Arg
 595 600 605

Gln Thr Ile Ser Phe Pro Pro Arg Asp Glu Trp Asn Asp Phe Asn Phe
610 615 620

Asp Met Asp Ala Arg Arg Asn Lys Gln Gln Arg Ile Lys Glu Glu Gly
625 630 635 640

Glu

<210> 7
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Descrip. of Artificial Sequence: p73-F1 sense primer

<400> 7
tacgtgcacg taaagacacg ttgctcc 27

<210> 8
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Descrip. of Artificial Sequence: p73-R1 antisense primer

<400> 8
tgctgcacgt tgctccacgt ggacgtacg 29

<210> 9
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Descrip. of Artificial Sequence: p73-F2 sense primer

<400> 9
tacgtatact acgacgtgta cgtgaaggg 29

<210> 10
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
 <223> Descrip. of Artificial Sequence: p73-R2 antisense primer

 <400> 10
 atgaactacg acgtacgacg tccacgtat 29

 <210> 11
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Descrip. of Artificial Sequence: HA-labeled expression construct

 <400> 11
 atgtatccat atgatgttcc agattatgct 30

 <210> 12
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Descrip. of Artificial Sequence: p51-F1 sense primer

 <400> 12
 aaagaaagtt attaccgatg 20

 <210> 13
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Descrip. of Artificial Sequence: p51-R1 antisense primer

 <400> 13
 cgcgtggtct gtgttatagg 20

 <210> 14
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Descrip. of Artificial Sequence: p51-F2 sense primer

 <400> 14
 catggaccag cagattcaga 20

<210> 15
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Descrip. of Artificial Sequence: p51-R2 antisense primer

 <400> 15
 catcaccttg atctggatg 19

 <210> 16
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Descrip. of Artificial Sequence: p51-F3 sense primer

 <400> 16
 ccacctggac gtattccact 20

 <210> 17
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Descrip. of Artificial Sequence: p51-R3 antisense primer

 <400> 17
 tggctcataa ggtaccag 18

 <210> 18
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Descrip. of Artificial Sequence: p51-F4 sense primer

 <400> 18
 catgagctga gccgtgaat 19

 <210> 19
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Descrip. of Artificial Sequence: p51-R4 antisense primer

<400> 19
 tatcttcatc cgccttcctg 20

<210> 20
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Descrip. of Artificial Sequence: p51-F5 sense primer

<400> 20
 atgaaccgcc gtccaatt 18

<210> 21
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Descrip. of Artificial Sequence: p51-R5 antisense primer

<400> 21
 gtgctgagga aggtactgca 20

<210> 22
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Descrip. of Artificial Sequence: p51-F6 sense primer

<400> 22
 tgaagatcaa agagtccttg 20

<210> 23
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Descrip. of Artificial Sequence: p51-R6 antisense primer

<400> 23
 ctagtggtt tgtgcctttg 20